



OIPE

RAW SEQUENCE LISTING

DATE: 06/16/2004

PATENT APPLICATION: US/10/055,536

TIME: 11:23:52

Input Set : N:\Cr3\RULE60\10055536.raw

Output Set: N:\CRF4\06162004\J055536.raw

1 <110> APPLICANT: DUTTA, Sukanta K.
 2 BISWAS, Biswajit
 3 VEMULAPALLI, Ramesh
 4 <120> TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR
 5 POTOMAC HORSE FEVER
 6 <130> FILE REFERENCE: 8172-9016
 7 <140> CURRENT APPLICATION NUMBER: US/10/055,536
 8 <141> CURRENT FILING DATE: 2002-01-23
 9 <150> PRIOR APPLICATION NUMBER: US/09/157,257
 10 <151> PRIOR FILING DATE: 1998-09-18
 11 <150> PRIOR APPLICATION NUMBER: 60/059,252
 12 <151> PRIOR FILING DATE: 1997-09-18
 13 <160> NUMBER OF SEQ ID NOS: 48
 14 <170> SOFTWARE: PatentIn Ver. 2.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 33
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 20 <220> FEATURE:
 21 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 22 primer
 23 <400> SEQUENCE: 1
 24 cataaaattt ctaagacgaa ggatccctat gtc 33
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 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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 37 <211> LENGTH: 2836
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Ehrlichia risticii
 40 <220> FEATURE:
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 42 <222> LOCATION: (175)..(2721)
 43 <400> SEQUENCE: 3
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 45 ttaaatttta tgatttttta taataaaaat agatataaaa tttagtagtt ttataaattt 120
 46 ttcataacaa aggactatcc tccttgcata aaatttctaa gacgaaaaat ccct atg 177

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Output Set: N:\CRF4\06162004\J055536.raw

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47                                     Met
48                                     1
49      tca aat gaa aca ctt ttg agc gta ctt tct gat gaa acg cac ttt gct 225
50      Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
51               5                10                15
52      aat cta gtt gat gaa ctt ctt ctc atc ttg gtt aaa gac agt att ttc 273
53      Asn Leu Val Asp Glu Leu Leu Leu Ile Leu Val Lys Asp Ser Ile Phe
54               20                25                30
55      act caa gta ata aaa ggc gag gga aag aca gaa tta aaa gac ata ctt 321
56      Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
57               35                40                45
58      aca gac aac act ggt aag ttt aaa gaa ctt ata gaa agt gca ggt aaa 369
59      Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys
60               50                55                60                65
61      gac ata cta aaa gag ata ctt aca gac aat acc ggc aat ttt aaa gga 417
62      Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly
63               70                75                80
64      ctt ata gaa ggt aat ggt aag acg gag gca aaa gag gta cgc act aat 465
65      Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr Asn
66               85                90                95
67      gaa aaa ttc aag gag ctt ttt gga agc aat ggt aag gac ata ctg aaa 513
68      Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu Lys
69               100               105               110
70      gac att ctt act gat aac acc ggt aac ttt aaa ggc ctt ata gaa agt 561
71      Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser
72               115               120               125
73      gca gct aag ggt aag ctg aaa gat ctt ctt att gat gaa aaa ttt caa 609
74      Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe Gln
75               130               135               140               145
76      aaa tta ttc gag gat gaa acg aaa gct ggt cgt gta aaa gaa ata ctt 657
77      Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile Leu
78               150               155               160
79      aca gac agc aac gct aag gaa ata ctc aca aat gaa gta gca aaa gag 705
80      Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu
81               165               170               175
82      gta cta aaa tcc gat aaa ttc aag gag gca ata act ggc gat ggt aag 753
83      Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly Lys
84               180               185               190
85      gac gca cta aaa gag ata ctt act tgt gat aaa ttt aaa gag gct gta 801
86      Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val
87               195               200               205
88      aca ggc aat ggt aaa gac ata cta aaa ggt ata ctt aca gat agc act 849
89      Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr
90               210               215               220               225
91      ggt aaa ttt aaa gaa ctt ata gaa agt act agt aaa gac ata cta aaa 897
92      Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Ser Lys Asp Ile Leu Lys
93               230               235               240
94      gag ata ctt aca gat aat acc ggt aac ttt aaa ggc ctt ata gaa agc 945
95      Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser

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96		245		250		255		
97	act ggc aag gag aaa gta aaa gaa ctt ctt atc gat ggg aag ttt aag							993
98	Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe Lys							
99		260		265		270		
100	gac ctg ttt act gat gca aca aaa gcc ggt tat gta aaa gaa ata ctc							1041
101	Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu							
102		275		280		285		
103	acg aac gat aca gct aag gaa gta ctt aca gat caa aca gca aag gag							1089
104	Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Gln Thr Ala Lys Glu							
105		290		295		300		305
106	gtc cta aaa gat agt aca gct aaa gac ata tta aag gac aca aac gca							1137
107	Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala							
108			310		315		320	
109	gct gcg gta cta aaa aac agc aca gct aaa gaa ata ctt aca aac caa							1185
110	Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn Gln							
111			325		330		335	
112	acc gct aaa gaa gtg ctt aca gat ggt aca tcc aaa gaa gta cta aaa							1233
113	Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu Lys							
114		340		345		350		
115	gag ata ctt act tgt gat aaa ttt aaa gag gca gta aca gga gat ggt							1281
116	Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp Gly							
117		355		360		365		
118	aaa gac ata cta aaa ggt ata ctt aca gat agc act ggt aag ttt aaa							1329
119	Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys							
120		370		375		380		385
121	gaa ctt ata gaa agt act ggt aaa gac ata ctg aaa gac att ctt aca							1377
122	Glu Leu Ile Glu Ser Thr Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr							
123			390		395		400	
124	gat agc act ggt aaa ttt aaa gaa ctt ata gaa gta ctg gta aag aac							1425
125	Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys Asn							
126		405		410		415		
127	aag cta aaa gag att ctt aca gat aac acc ggt aac ttc aaa ggg ctt							1473
128	Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu							
129		420		425		430		
130	gta gaa ggc gcc ggg aag gat gaa gca aaa gca gta ctt act gac gag							1521
131	Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp Glu							
132		435		440		445		
133	aaa ttt aaa ggc ttg ttt gat gac aaa aca ata gct ggc tat gta aaa							1569
134	Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys							
135		450		455		460		465
136	gaa ata ctc acc agc gag aag ttt aaa aaa ctg ttt gaa agt gca ggt							1617
137	Glu Ile Leu Thr Ser Glu Lys Phe Lys Lys Leu Phe Glu Ser Ala Gly							
138			470		475		480	
139	aag act aaa gta aaa gaa ctc ctc att gat gag aag ttt caa aaa tta							1665
140	Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu							
141		485		490		495		
142	ttt gag gat gac acg aaa gcc agt cat gta aaa gaa ata ctc acg aac							1713
143	Phe Glu Asp Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asn							
144		500		505		510		

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145	gat aca gct aag gaa ata ctt aca gat caa aca gct aaa gaa gtc cta	1761
146	Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu Val Leu	
147	515 520 525	
148	aag gat agt aca gct aaa gag ata tta aag gac aca aac gca gct gcg	1809
149	Lys Asp Ser Thr Ala Lys Glu Ile Leu Lys Asp Thr Asn Ala Ala Ala	
150	530 535 540 545	
151	cta cta aaa gac agc aca gca aaa gag gta cta aaa tcc gat aaa ttt	1857
152	Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Ser Asp Lys Phe	
153	550 555 560	
154	aaa gat gca ata act ggt gct ggt aag gac gca cta aaa gag ata ctt	1905
155	Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu	
156	565 570 575	
157	act tgt gat aaa ttt aaa gag gca gta aca ggc aat ggt aaa gac ata	1953
158	Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asn Gly Lys Asp Ile	
159	580 585 590	
160	cta aaa ggt ata ctt aca gat agc act ggt aaa ttt aaa gag cta ata	2001
161	Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile	
162	595 600 605	
163	gaa agc act ggt aag gat aag cta aaa gag att ctt aca gat aac acc	2049
164	Glu Ser Thr Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr	
165	610 615 620 625	
166	ggt aac ttt aaa ttt ctt gta gaa ggc gcc ggt aag gat gaa gca aaa	2097
167	Gly Asn Phe Lys Phe Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys	
168	630 635 640	
169	gca gta ctt act cac gag aaa ttt aaa gac ttg ttt aat gtc aaa aca	2145
170	Ala Val Leu Thr His Glu Lys Phe Lys Asp Leu Phe Asn Val Lys Thr	
171	645 650 655	
172	aca gct ggc tac gtg aaa gaa ata ctt acc agc gac aag ttt aaa gaa	2193
173	Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Glu	
174	660 665 670	
175	ctg ttt act gat gca aca aaa gct ggc tac gtg aaa gaa ata ctc acg	2241
176	Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr	
177	675 680 685	
178	aac gat aca gct aag gaa ata ctt aca gat caa aca gct aaa gaa gtc	2289
179	Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu Val	
180	690 695 700 705	
181	cta aag gat ggt aca gct aaa gac ata tta aag gac aca aac gca cgt	2337
182	Leu Lys Asp Gly Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala Arg	
183	710 715 720	
184	gcg cta cta aaa gac agc aca gcc aaa gaa gta cta aaa tgc gat aaa	2385
185	Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Cys Asp Lys	
186	725 730 735	
187	ttt aag gaa gca ata aca ggt gcc ggt aaa gat gag cta aaa tac ata	2433
188	Phe Lys Glu Ala Ile Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile	
189	740 745 750	
190	ctc act aat agc gag ttt aaa agc tta ttt cat agc aaa gat agc gct	2481
191	Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe His Ser Lys Asp Ser Ala	
192	755 760 765	
193	gaa gct gtt aaa gca ata ttt acc cac aat aag ttt aaa gaa cta ctt	2529

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197   Glu His Ala Arg Thr Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn Ala
198                               790                               795                               800
199   tta gat caa cta aaa gcg cta att acc tgt ggc agc ggt gat cat gca   2625
200   Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His Ala
201                               805                               810                               815
202   aca aaa cta caa gcc ttt gga agt gca cta tgc acc aaa aag aag gag   2673
203   Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys Glu
204                               820                               825                               830
205   ttg tgc agt aat ttt agc tgt gca aac tgc agt agt aca aca act gca   2721
206   Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr Ala
207   835                               840                               845
208   taattacgta gcgctagggtg ggggtaattt acccccacct agctagaatc acacgggggaa 2781
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212 <211> LENGTH: 849
213 <212> TYPE: PRT
214 <213> ORGANISM: Ehrlichia risticii
215 <400> SEQUENCE: 4
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220   Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
221   35                               40                               45
222   Leu Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly
223   50                               55                               60
224   Lys Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys
225   65                               70                               75                               80
226   Gly Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr
227   85                               90                               95
228   Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu
229   100                              105                              110
230   Lys Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
231   115                              120                              125
232   Ser Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe
233   130                              135                              140
234   Gln Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile
235   145                              150                              155                              160
236   Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys
237   165                              170                              175
238   Glu Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly
239   180                              185                              190
240   Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala
241   195                              200                              205
242   Val Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser
243   210                              215                              220

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:17

VERIFICATION SUMMARY

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Input Set : N:\CrF3\RULE60\10055536.raw

Output Set: N:\CRF4\06162004\J055536.raw

L:775 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence

L:775 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence

L:775 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:775